



#7

SEQUENCE LISTING

GENERAL INFORMATION:

(i) APPLICANT: Anderson, Darrell R.
Hanna, Nabil
Leonard, John E.
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Reff, Mitchell E.
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(ii) TITLE OF INVENTION: Therapeutic Application of Chimeric and Radiolabeled Antibodies to Human B Lymphocyte Restricted Differentiation Antigen for the Treatment of B-Cell Lymphoma

(iii) NUMBER OF SEQUENCES: 11

(iv) CORRESPONDENCE ADDRESS:

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(C) CITY: Alexandria
(D) STATE: VA
(E) COUNTRY: USA
(F) ZIP: 22314

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/476,275
(B) FILING DATE: 07-JUN-1995
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/149,099
(B) FILING DATE: 03-NOV-1993

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/978,891
(B) FILING DATE: 13-NOV-1992

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Teskin, Robin L.
(B) REGISTRATION NUMBER: 35,030
(C) REFERENCE/DOCKET NUMBER: 012712-155

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: TCAE 8

9 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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GGGGAGCCTG GGGACTTTCC ACACCCTAAC TGACACACAT TCCACAGAAT TAATTCCCCT	360
AGTTATTAAT AGTAATCAAT TACGGGGTCA TTAGTTCATA GCCCATATAT GGAGTTCCGC	420
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TTCCTACTTG	GCAGTACATC	TACGTATTAG	TCATCGCTAT	TACCATGGTG	ATGCGGTTTT	1860
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GCCTGATTCC	GTAGAGCCAC	ACCTTGGTAA	GGGCCAATCT	GCTCACACAG	GATAGAGAGG	3780
CAGGAGCCAG	GGCAGAGCAT	ATAAGGTGAG	GTAGGATCAG	GTTGCTCCTC	ACATTTGCTT	3840
CTGACATAGT	TGTGTTGGGA	CGTTGGATAG	CTTGGACAGC	TCAGGGCTGC	GATTTCGCGC	3900
CAAACCTGAC	GGCAATCCTA	GCGTGAAGGC	TGGTAGGATT	TTATCCCCGC	TGCCATCATG	3960
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CCTGAGAAGA	ATCGACCTTT	AAAGGACAGA	ATTAATATAG	TTCTCAGTAG	AGAACTCAAA	4200
GAACCACCAC	GAGGAGCTCA	TTTTCTTGCC	AAAAGTTTGG	ATGATGCCTT	AAGACTTATT	4260
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TGCCACTCCC	ACTGTCCTTT	CCTAATAAAA	TGAGGAAATT	GCATCGCATT	GTCTGAGTAG	4740
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CAATAGCAGG	CATGCTGGGG	ATGCGGTGGG	CTCTATGGAA	CCAGCTGGGG	CTCGAGCTAC	4860
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GCTGCTATTG	GGCGAAGTGC	CGGGGCAGGA	TCTCCTGTCA	TCTCACCTTG	CTCCTGCCGA	5580
GAAAGTATCC	ATCATGGCTG	ATGCAATGCG	GCGGCTGCAT	ACGCTTGATC	CGGCTACCTG	5640
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CGCCAGGCTC	AAGGCGCGCA	TGCCCCGACG	CGAGGATCTC	GTCGTGACCC	ATGGCGATGC	5820
CTGCTTGCCG	AATATCATGG	TGGAAAATGG	CCGCTTTTCT	GGATTCATCG	ACTGTGGCCG	5880
GCTGGGTGTG	GCGGACCGCT	ATCAGGACAT	AGCGTTGGCT	ACCCGTGATA	TTGCTGAAGA	5940
GCTTGCGGCG	GAATGGGCTG	ACCGCTTCCT	CGTGCTTTAC	GGTATCGCCG	CTTCCCGATT	6000
CGCAGCGCAT	CGCCTTCTAT	CGCCTTCTTG	ACGAGTTCTT	CTGAGCGGGA	CTCTGGGGTT	6060

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CGAAATGACC	GACCAAGCGA	CGCCCAACCT	GCCATCACGA	GATTTTCGATT	CCACCGCCGC	6120
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GCGCGGGGAT	CTCATGCTGG	AGTTCTTCGC	CCACCCCAAC	TTGTTTATTG	CAGCTTATAA	6240
TGGTTACAAA	TAAAGCAATA	GCATCACAAA	TTTCACAAAT	AAAGCATTTT	TTTCACTGCA	6300
TTCTAGTTGT	GGTTTGTCCA	AACTCATCAA	TCTATCTTAT	CATGTCTGGA	TCGCGGCCGC	6360
GATCCCGTCG	AGAGCTTGGC	GTAATCATGG	TCATAGCTGT	TTCTGTGTG	AAATTGTTAT	6420
CCGCTCACAA	TTCCACACAA	CATACGAGCC	GGAAGCATAA	AGTGTAAGC	CTGGGGTGCC	6480
TAATGAGTGA	GCTAACTCAC	ATTAATTGCG	TTGCGCTCAC	TGCCCCGCTTT	CCAGTCGGGA	6540
AACCTGTCGT	GCCAGCTGCA	TTAATGAATC	GGCCAACGCG	CGGGGAGAGG	CGGTTTGCGT	6600
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GTCGTTTCGCT	CCAAGCTGGG	CTGTGTGCAC	GAACCCCCCG	TTCAGCCCGA	CCGCTGCGCC	7080
TTATCCGGTA	ACTATCGTCT	TGAGTCCAAC	CCGGTAAGAC	ACGACTTATC	GCCACTGGCA	7140
GCAGCCACTG	GTAACAGGAT	TAGCAGAGCG	AGGTATGTAG	GCGGTGCTAC	AGAGTTCTTG	7200
AAGTGGTGGC	CTAACTACGG	CTACACTAGA	AGGACAGTAT	TTGGTATCTG	CGCTCTGCTG	7260
AAGCCAGTTA	CCTTCGGAAA	AAGAGTTGGT	AGCTCTTGAT	CCGGCAAACA	AACCACCGCT	7320
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GAAGATCCTT	TGATCTTTTC	TACGGGGTCT	GACGCTCAGT	GGAACGAAAA	CTCACGTTAA	7440
GGGATTTTGG	TCATGAGATT	ATCAAAAAGG	ATCTTCACCT	AGATCCTTTT	AAATTAAAAA	7500
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TGAGCAAAAA CAGGAAGGCA AAATGCCGCA AAAAAGGGAA TAAGGGCGAC ACGGAAATGT	8400
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TTCCCCGAA AAGTGCCACC T	8541

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: anti-CD20 in TCAE 8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GACGTCGCGG CCGCTCTAGG CCTCAAAAAA AGCCTCCTCA CTA CTCTCTGG AATAGCTCAG	60
AGGCCGAGGC GGCCTCGGCC TCTGCATAAA TAAAAAAAAT TAGTCAGCCA TGCATGGGGC	120
GGAGAATGGG CGGAACTGGG CGGAGTTAGG GGCGGGATGG GCGGAGTTAG GGGCGGGACT	180

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GACTTTCCAC	ACCTGGTTGC	TGACTAATTG	AGATGCATGC	TTTGCATACT	TCTGCCTGCT	300
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GCATCTCCAG	GGGAGAAGGT	CACAATGACT	TGCAGGGCCA	GCTGAAGTGT	AAGTTACATC	1140
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GGACTCTACT	CCCTCAGCAG	CGTGGTGACC	GTGCCCTCCA	GCAGCTTGGG	CACCCAGACC	3060
TACATCTGCA	ACGTGAATCA	CAAGCCCAGC	AACACCAAGG	TGGACAAGAA	AGCAGAGCCC	3120
AAATCTTG TG	ACAAAAC TCA	CACATGCCCA	CCGTGCCCAG	CACCTGAACT	CCTGGGGGGA	3180
CCGTCAGTCT	TCCTCTTCCC	CCCAAACCC	AAGGACACCC	TCATGATCTC	CCGGACCCCT	3240
GAGGTCACAT	GCGTG GTGGT	GGACGTGAGC	CACGAAGACC	CTGAGGTCAA	GTTCAACTGG	3300
TACGTGGACG	GCGTG GAGGT	GCATAATGCC	AAGACAAAGC	CGCGGGAGGA	GCAGTACAAC	3360
AGCACGTACC	GTGTGGTCAG	CGTCCTCACC	GTCTGTCACC	AGGACTGGCT	GAATGGCAAG	3420
GAGTACAAGT	GCAAGGTCTC	CAACAAAGCC	CTCCCAGCCC	CCATCGAGAA	AACCATCTCC	3480
AAAGCCAAAG	GGCAGCCCCG	AGAACCACAG	GTGTACACCC	TGCCCCCATC	CCGGGATGAG	3540

CTGACCAAGA	ACCAGGTCAG	CCTGACCTGC	CTGGTCAAAG	GCTTCTATCC	CAGCGACATC	3600
GCCGTGGAGT	GGGAGAGCAA	TGGGCAGCCG	GAGAACAAC	ACAAGACCAC	GCCTCCCGTG	3660
CTGGACTCCG	ACGGCTCCTT	CTTCCTCTAC	AGCAAGCTCA	CCGTGGACAA	GAGCAGGTGG	3720
CAGCAGGGGA	ACGTCTTCTC	ATGCTCCGTG	ATGCATGAGG	CTCTGCACAA	CCACTACACG	3780
CAGAAGAGCC	TCTCCCTGTC	TCCGGGTAAA	TGAGGATCCG	TTAACGGTTA	CCAACCTACCT	3840
AGACTGGATT	CGTGACAACA	TGCGGCCGTG	ATATCTACGT	ATGATCAGCC	TCGACTGTGC	3900
CTTCTAGTTG	CCAGCCATCT	GTTGTTTGCC	CCTCCCCCGT	GCCTTCCTTG	ACCCTGGAAG	3960
GTGCCACTCC	CACTGTCCTT	TCCTAATAAA	ATGAGGAAAT	TGCATCGCAT	TGTCTGAGTA	4020
GGTGTCAATC	TATTCTGGGG	GGTGGGGTGG	GGCAGGACAG	CAAGGGGGAG	GATTGGGAAG	4080
ACAATAGCAG	GCATGCTGGG	GATGCGGTGG	GCTCTATGGA	ACCAGCTGGG	GCTCGACAGC	4140
GCTGGATCTC	CCGATCCCCA	GCTTTGCTTC	TCAATTTCTT	ATTTGCATAA	TGAGAAAAAA	4200
AGGAAAATTA	ATTTTAACAC	CAATTCAGTA	GTTGATTGAG	CAAATGCGTT	GCCAAAAAGG	4260
ATGCTTTAGA	GACAGTGGTC	TCTGCACAGA	TAAGGACAAA	CATTATTCAG	AGGGAGTACC	4320
CAGAGCTGAG	ACTCCTAAGC	CAGTGAGTGG	CACAGCATTC	TAGGGAGAAA	TATGCTTGTC	4380
ATCACCGAAG	CCTGATTCCG	TAGAGCCACA	CCTTGGTAAG	GGCCAATCTG	CTCACACAGG	4440
ATAGAGAGGG	CAGGAGCCAG	GGCAGAGCAT	ATAAGGTGAG	GTAGGATCAG	TTGCTCCTCA	4500
CATTTGCTTC	TGACATAGTT	GTGTTGGGAG	CTTGGATAGC	TTGGACAGCT	CAGGGCTGCG	4560
ATTTGCGGCC	AAACTTGACG	GCAATCCTAG	CGTGAAGGCT	GGTAGGATTT	TATCCCCGCT	4620
GCCATCATGG	TTCGACCATT	GAAGTGCATC	GTCGCCGTGT	CCCAAATAT	GGGGATTGGC	4680
AAGAACGGAG	ACCTACCCTG	GCCTCCGCTC	AGGAACGAGT	TCAAGTACTT	CCAAAGAATG	4740
ACCACAACCT	CTTCAGTGGA	AGGTAAACAG	AATCTGGTGA	TTATGGGTAG	GAAAACCTGG	4800
TTCTCCATTC	CTGAGAAGAA	TCGACCTTTA	AAGGACAGAA	TTAATATAGT	TCTCAGTAGA	4860
GAACTCAAAG	AACCACCACG	AGGAGCTCAT	TTTCTTGCCA	AAAGTTTGGA	TGATGCCTTA	4920
AGACTTATTG	AACAACCGGA	ATTGGCAAGT	AAAGTAGACA	TGGTTTGAT	AGTCGGAGGC	4980
AGTTCTGTTT	ACCAGGAAGC	CATGAATCAA	CCAGGCCACC	TTAGACTCTT	TGTGACAAGG	5040
ATCATGCAGG	AATTTGAAAG	TGACACGTTT	TTCCCAGAAA	TTGATTTGGG	GAAATATAAA	5100
CTTCTCCCAG	AATACCCAGG	CGTCCTCTCT	GAGGTCCAGG	AGGAAAAAGG	CATCAAGTAT	5160
AAGTTTGAAG	TCTACGAGAA	GAAAGACTAA	CAGGAAGATG	CTTTCAAGTT	CTCTGCTCCC	5220

CTCCTAAAGC	TATGCATTTT	TATAAGACCA	TGGGACTTTT	GCTGGCTTTA	GATCAGCCTC	5280
GACTGTGCCT	TCTAGTTGCC	AGCCATCTGT	TGTTTGCCCC	TCCCCCGTGC	CTTCCTTGAC	5340
CCTGGAAGGT	GCCACTCCCA	CTGTCCTTTC	CTAATAAAAT	GAGGAAATTG	CATCGCATTG	5400
TCTGAGTAGG	TGTCATTCTA	TTCTGGGGGG	TGGGGTGGGG	CAGGACAGCA	AGGGGGAGGA	5460
TTGGGAAGAC	AATAGCAGGC	ATGCTGGGGA	TGCGGTGGGC	TCTATGGAAC	CAGCTGGGGC	5520
TCGAGCTACT	AGCTTTGCTT	CTCAATTTCT	TATTTGCATA	ATGAGAAAAA	AAGGAAAATT	5580
AATTTTAACA	CCAATTCAGT	AGTTGATTGA	GCAAATGCGT	TGCCAAAAAG	GATGCTTTAG	5640
AGACAGTGTT	CTCTGCACAG	ATAAGGACAA	CTAGGGAGAA	ATATGCTTGT	CATCACCGAA	5700
GACTCCTAAG	CCAGTGAGTG	GCACAGCATT	CTAGGGAGAA	ATATGCTTGT	CATCACCGAA	5760
GCCTGATTCC	GTAGAGCCAC	ACCTTGGTAA	GGGCCAATCT	GCTCACACAG	GATAGAGAGG	5820
GCAGGAGCCA	GGGCAGAGCA	TATAAGGTGA	GGTAGGATCA	GTTGCTCCTC	ACATTTGCTT	5880
CTGACATAGT	TGTGTTGGGA	GCTTGGATCG	ATCCTCTATG	GTTGAACAAG	ATGGATTGCA	5940
CGCAGGTTCT	CCGGCCGCTT	GGGTGGAGAG	GCTATTCGGC	TATGACTGGG	CACAACAGAC	6000
AATCGGCTGC	TCTGATGCCG	CCGTGTTCCG	GCTGTCAGCG	CAGGGGCGCC	CGGTTCTTTT	6060
TGTCAAGACC	GACCTGTCCG	GTGCCCTGAA	TGAACTGCAG	GACGAGGCAG	CGCGGCTATC	6120
GTGGCTGGCC	ACGACGGGCG	TTCCTTGCGC	AGCTGTGCTC	GACGTTGTCA	CTGAAGCGGG	6180
AAGGGACTGG	CTGCTATTGG	GCGAAGTGCC	GGGGCAGGAT	CTCCTGTCA	CTCACCTTGC	6240
TCCTGCCGAG	AAAGTATCCA	TCATGGCTGA	TGCAATGCGG	CGGCTGCATA	CGCTTGATCC	6300
GGCTACCTGC	CCATTCGACC	ACCAAGCGAA	ACATCGCATC	GAGCGAGCAC	GTACTCGGAT	6360
GGAAGCCGGT	CTTGTCGATC	AGGATGATCT	GGACGAAGAG	CATCAGGGGC	TCGCGCCAGC	6420
CGAACTGTTC	GCCAGGCTCA	AGGCGCGCAT	GCCCGACGGC	GAGGATCTCG	TCGTGACCCA	6480
TGGCGATGCC	TGCTTGCCGA	ATATCATGGT	GGAAAATGGC	CGCTTTTCTG	GATTCATCGA	6540
CTGTGGCCGG	CTGGGTGTGG	CGGACCGCTA	TCAGGACATA	GCGTTGGCTA	CCCGTGATAT	6600
TGCTGAAGAG	CTTGCCGGCG	AATGGGCTGA	CCGCTTCCTC	GTGCTTTACG	GTATCGCCGC	6660
TCCCGATTCTG	CAGCGCATCG	CCTTCTATCG	CCTTCTTGAC	GAGTTCTTCT	GAGCGGGACT	6720
CTGGGGTTCTG	AAATGACCGA	CCAAGCGACG	CCCAACCTGC	CATCACGAGA	TTTCGATTCC	6780
ACCGCCGCCT	TCTATGAAAG	GTTGGGCTTC	GGAATCGTTT	TCCGGGACGC	CGGCTGGATG	6840
ATCCTCCAGC	GCGGGGATCT	CATGCTGGAG	TTCTTCGCCC	ACCCAACTT	GTTTATTGCA	6900

GCTTATAATG	GTTACAAATA	AAGCAATAGC	ATCACAAATT	TCACAAATAA	AGCATTTTTT	6960
TCACTGCATT	CTAGTTGTGG	TTTGTCCAAA	CTCATCAATC	TATCTTATCA	TGTCTGGATC	7020
GCGGCCGCGA	TCCCGTCGAG	AGCTTGGCGT	AATCATGGTC	ATAGCTGTTT	CCTGTGTGAA	7080
ATTGTTATCC	GCTCACAATT	CCACACAACA	TACGAGCCGG	AAGCATAAAG	TGTAAAGCCT	7140
GGGGTGCCTA	ATGAGTGAGC	TAACTCACAT	TAATTGCGTT	GCGCTCACTG	CCCGCTTTCC	7200
AGTCGGGAAA	CCTGTCGTGC	CAGCTGCATT	AATGAATCGG	CCAACGCGCG	GGGAGAGGCG	7260
GTTTGCGTAT	TGGGCGCTCT	TCCGCTTCCT	CGCTCACTGA	CTCGCTGCGC	TCGGTCGTTC	7320
GGCTGCGGCG	AGCGGTATCA	GCTCACTCAA	AGGCGGTAAT	ACGGTTATCC	ACAGAATCAG	7380
GGGATAACGC	AGGAAAGAAC	ATGTGAGCAA	AAGGCCAGCA	AAAGGCCAGG	AACCGTAAAA	7440
AGGCCGCGTT	GCTGGCGTTT	TTCCATAGGC	TCCGCCCCCC	TGACGAGCAT	CACAAAAATC	7500
GACGCTCAAG	TCAGAGGTGG	CGAAACCCGA	CAGGACTATA	AAGATACCAG	GCGTTTCCCC	7560
CTGGAAGCTC	CCTCGTGCGC	TCTCCTGTTC	CGACCCTGCC	GCTTACCGGA	TACCTGTCCG	7620
CCTTTCTCCC	TTCGGGAAGC	GTGGCGCTTT	CTCAATGCTC	ACGCTGTAGG	TATCTCAGTT	7680
CGGTGTAGGT	CGTTCGCTCC	AAGCTGGGCT	GTGTGCACGA	ACCCCCGTT	CAGCCCGACC	7740
C1 GCTGCGCCTT	ATCCGGTAAC	TATCGTCTTG	AGTCCAACCC	GGTAAGACAC	GACTTATCGC	7800
CACTGGCAGC	AGCCACTGGT	AACAGGATTA	GCAGAGCGAG	GTATGTAGGC	GGTGCTACAG	7860
AGTTCTTGAA	GTGGTGGCCT	AACTACGGCT	ACACTAGAAG	GACAGTATTT	GGTATCTGCG	7920
CTCTGCTGAA	GCCAGTTACC	TTCGGA AAAA	GAGTTGGTAG	CTCTTGATCC	GGCAAACAAA	7980
CCACCGCTGG	TAGCGGTGGT	TTTTTTGTTT	GCAAGCAGCA	GATTACGCGC	AGAAAAAAG	8040
GATCTCAAGA	AGATCCTTTG	ATCTTTTCTA	CGGGGTCTGA	CGCTCAGTGG	AACGAAAAC	8100
CACGTTAAGG	GATTTTGGTC	ATGAGATTAT	CAAAAAGGAT	CTTCACCTAG	ATCCTTTTAA	8160
ATTAAAAATG	AAGTTT TAAA	TCAATCTAAA	GTATATATGA	GTAAACTTGG	TCTGACAGTT	8220
ACCAATGCTT	AATCAGTGAG	GCACCTATCT	CAGCGATCTG	TCTATTTTCG	TCATCCATAG	8280
TTGCCTGACT	CCCCGTCGTG	TAGATAACTA	CGATACGGGA	GGGCTTACCA	TCTGGCCCCA	8340
GTGCTGCAAT	GATACGCGA	GACCCACGCT	CACCGGCTCC	AGATTTATCA	GCAATAAACC	8400
AGCCAGCCGG	AAGGGCCGAG	CGCAGAAGTG	GTCCTGCAAC	TTTATCCGCC	TCCATCCAGT	8460
CTATTAATTG	TTGCCGGGAA	GCTAGAGTAA	GTAGTTCGCC	AGTTAATAGT	TTGCGCAACG	8520
TTGTTGCCAT	TGCTACAGGC	ATCGTGGTGT	CACGCTCGTC	GTTTGGTATG	GCTTCATTCA	8580

GCTCCGGTTC CCAACGATCA AGGCGAGTTA CATGATCCCC CATGTTGTGC AAAAAAGCGG	8640
TTAGCTCCTT CGGTCCTCCG ATCGTTGTCA GAAGTAAGTT GGCCGCAGTG TTATCACTCA	8700
TGGTTATGGC AGCACTGCAT AATTCTCTTA CTGTCATGCC ATCCGTAAGA TGCTTTTCTG	8760
TGACTGGTGA GTACTCAACC AAGTCATTCT GAGAATAGTG TATGCGGCGA CCGAGTTGCT	8820
CTTGCCCGGC GTCAATACGG GATAATACCG CGCCACATAG CAGAACTTTA AAAGTGCTCA	8880
TCATTGGAAA ACGTTCTTCG GGGCGAAAAC TCTCAAGGAT CTTACCGCTG TTGAGATCCA	8940
GGTCGATGTA ACCCACTCGT GCACCCAACT GATCTTCAGC ATCTTTTACT TTCACCAGCG	9000
TTTCTGGGTG AGCAAAAACA GGAAGGCAAA ATGCCGCAAA AAAGGGAATA AGGGCGACAC	9060
GGAAATGTTG AATACTCATA CTCTTCCTTT TTCAATATTA TTGAAGCATT TATCAGGGTT	9120
ATTGTCTCAT GAGCGGATAC ATATTTGAAT GTATTTAGAA AAATAAACAA ATAGGGGTTC	9180
CGCGCACATT TCCCCGAAAA GTGCCACCT	9209

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: murine variable region light chain

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..384

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 67..384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG GAT TTT CAG GTG CAG ATT ATC AGC TTC CTG CTA ATC AGT GCT TCA	48
Met Asp Phe Gln Val Gln Ile Ile Ser Phe Leu Leu Ile Ser Ala Ser	
-22 -20 -15 -10	
GTC ATA ATG TCC AGA GGA CAA ATT GTT CTC TCC CAG TCT CCA GCA ATC	96
Val Ile Met Ser Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile	
-5 1 5 10	
CTG TCT GCA TCT CCA GGG GAG AAG GTC ACA ATG ACT TGC AGG GCC AGC	144

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Leu	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser		
				15					20					25			
TCA	AGT	GTA	AGT	TAC	ATC	CAC	TGG	TTC	CAG	CAG	AAG	CCA	GGA	TCC	TCC		192
Ser	Ser	Val	Ser	Tyr	Ile	His	Trp	Phe	Gln	Gln	Lys	Pro	Gly	Ser	Ser		
			30					35					40				
CCC	AAA	CCC	TGG	ATT	TAT	GCC	ACA	TCC	AAC	CTG	GCT	TCT	GGA	GTC	CCT		240
Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro		
		45					50					55					
GTT	CGC	TTC	AGT	GGC	AGT	GGG	TCT	GGG	ACT	TCT	TAC	TCT	CTC	ACC	ATC		288
Val	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile		
	60					65					70						
AGC	AGA	GTG	GAG	GCT	GAA	GAT	GCT	GCC	ACT	TAT	TAC	TGC	CAG	CAG	TGG		336
Ser	Arg	Val	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp		
	75				80					85					90		
ACT	AGT	AAC	CCA	CCC	ACG	TTC	GGA	GGG	GGG	ACC	AAG	CTG	GAA	ATC	AAA		384
Thr	Ser	Asn	Pro	Pro	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys		
				95				100						105			

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Asp	Phe	Gln	Val	Gln	Ile	Ile	Ser	Phe	Leu	Leu	Ile	Ser	Ala	Ser		
-22		-20					-15					-10					
Val	Ile	Met	Ser	Arg	Gly	Gln	Ile	Val	Leu	Ser	Gln	Ser	Pro	Ala	Ile		
	-5					1				5					10		
Leu	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser		
				15					20					25			
Ser	Ser	Val	Ser	Tyr	Ile	His	Trp	Phe	Gln	Gln	Lys	Pro	Gly	Ser	Ser		
			30					35					40				
Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro		
		45					50					55					
Val	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile		
	60					65					70						
Ser	Arg	Val	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp		
	75				80					85					90		

TAT	TAC	TGT	GCA	AGA	TCG	ACT	TAC	TAC	GGC	GGT	GAC	TGG	TAC	TTC	AAT	384
Tyr	Tyr	Cys	Ala	Arg	Ser	Thr	Tyr	Tyr	Gly	Gly	Asp	Trp	Tyr	Phe	Asn	
95						100					105					

GTC	TGG	GGC	GCA	GGG	ACC	ACG	GTC	ACC	GTC	TCT	GCA					420
Val	Trp	Gly	Ala	Gly	Thr	Thr	Val	Thr	Val	Ser	Ala					
110					115					120						

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 140 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Gly	Trp	Ser	Leu	Ile	Leu	Leu	Phe	Leu	Val	Ala	Val	Ala	Thr	Arg	
-19				-15					-10					-5		
Val	Leu	Ser	Gln	Val	Gln	Leu	Gln	Gln	Pro	Gly	Ala	Glu	Leu	Val	Lys	
			1				5					10				
Ala	Gly	Ala	Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	
15						20					25					
Thr	Ser	Tyr	Asn	Met	His	Trp	Val	Lys	Gln	Thr	Pro	Gly	Arg	Gly	Leu	
30					35					40					45	
Glu	Trp	Ile	Gly	Ala	Ile	Tyr	Pro	Gly	Asn	Gly	Asp	Thr	Ser	Tyr	Asn	
				50					55						60	
Gln	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	Ser	Ser	Ser	
			65					70					75			
Thr	Ala	Tyr	Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	
		80					85					90				
Tyr	Tyr	Cys	Ala	Arg	Ser	Thr	Tyr	Tyr	Gly	Gly	Asp	Trp	Tyr	Phe	Asn	
95						100					105					
Val	Trp	Gly	Ala	Gly	Thr	Thr	Val	Thr	Val	Ser	Ala					
110					115					120						

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGGAGCTTGG ATCGATCCTC TATGGTT

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(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATCACAGATC TCTCACCATG GATTTTCAGG TGCAGATTAT CAGCTTC

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(2) INFORMATION FOR SEQ ID NO:9:

C (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGCAGCATCC GTACGTTTGA TTTCCAGCTT

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(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCGGCTCCCA CGCGTGTCCCT GTCCCAG

27

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGSTGTTGTG CTAGCTGMRG AGACRGTGA

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